Myelination Differences of Stripes in Human V2: Preliminary Evidence from 7 T Quantitative MRI

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Introduction

- The second visual area (V2) is known to contain a repeating pale-thin-pale-thick stripe pattern of cytochrome oxidase activity (CO). [1]
- Staining for myelin also reveals a stripe pattern in V2. However, it is still debated whether pale or dark stripes defined by CO are heavier myelinated. [2]
- Recent advances in ultra high field MRI enabled the functional delineation of V2 stripes *in vivo*. [3,4]
- In this study, we exploited the sensitivity of MRI to myelin and acquired high-resolution fMRI in conjunction with qMRI (R1, R2*) to infer myelination differences [5] between stripe types in humans.
- Our results show that V2 **pale stripes** are heavier myelinated than surrounding gray matter.

Methods

Experimental design

4 volunteers participated in several scanning sessions over multiple days. Thin and thick stripes were functionally localized by exploiting their different sensitivity to color and binocular disparity, respectively, see Fig. 1. [4] Relaxation parameters (R1, R2*) were determined from a high resolution MPM protocol. [6]

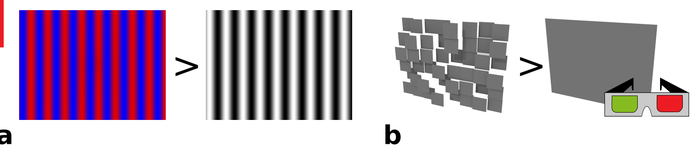
MRI data acquisition

Measurements were performed on a Siemens MAGNETOM 7 T whole-body MR scanner (Siemens, Germany) using a 32-channel RF coil (Nova Medical, USA). For fMRI, we acquired an oblique-coronal slab (50 slices) using a GE-EPI protocol (iso. 0.8 mm, TR = 3000 ms, TE = 24 ms, GRAPPA = 3, part. Fourier = 6/8). For qMRI, the MPM protocol consisted of 2 multi-echo FLASH acquisitions with T1- and PD-weighting (iso. 0.5 mm, 6 echoes, TR = 25 ms, TE = 2-16 ms. GRAPPA = 2x2) plus maps of B1+ and B0. An optical tracking system was used (Kineticor, USA) to prospectively correct head motion during anatomical scans.

Analysis

Cortex segmentation was performed with FreeSurfer (6.0.0) on a separately acquired MP2RAGE scan. QMRI parameter maps were computed using the hMRI toolbox [7]. SPM12 was used for fMRI processing.

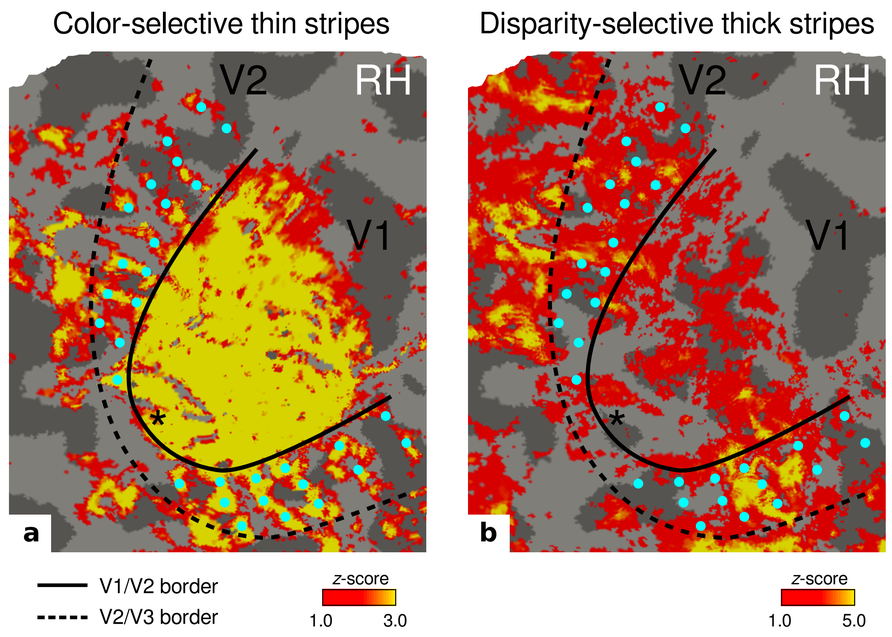
1



Visual stimuli — A block design with two experimental conditions was used to map thin (a) and tick (b) stripes in V2. Further details can be found in [4].

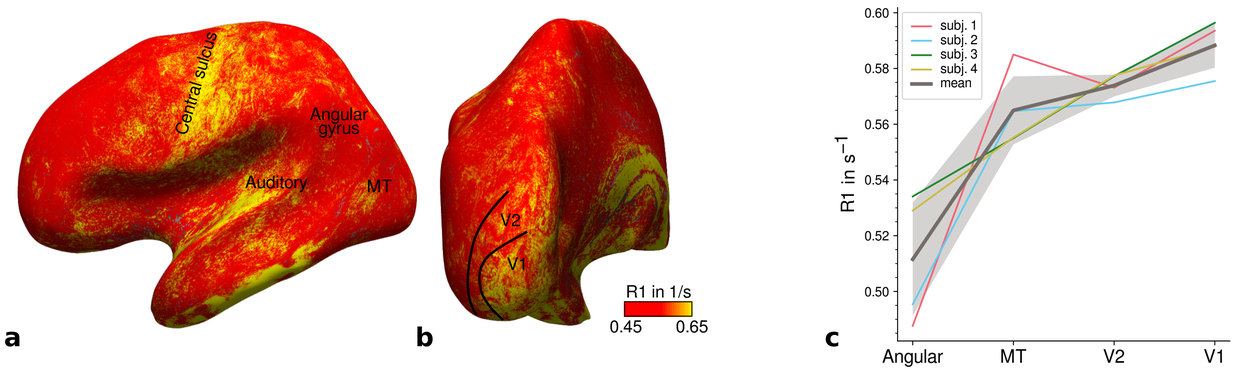
Results

2



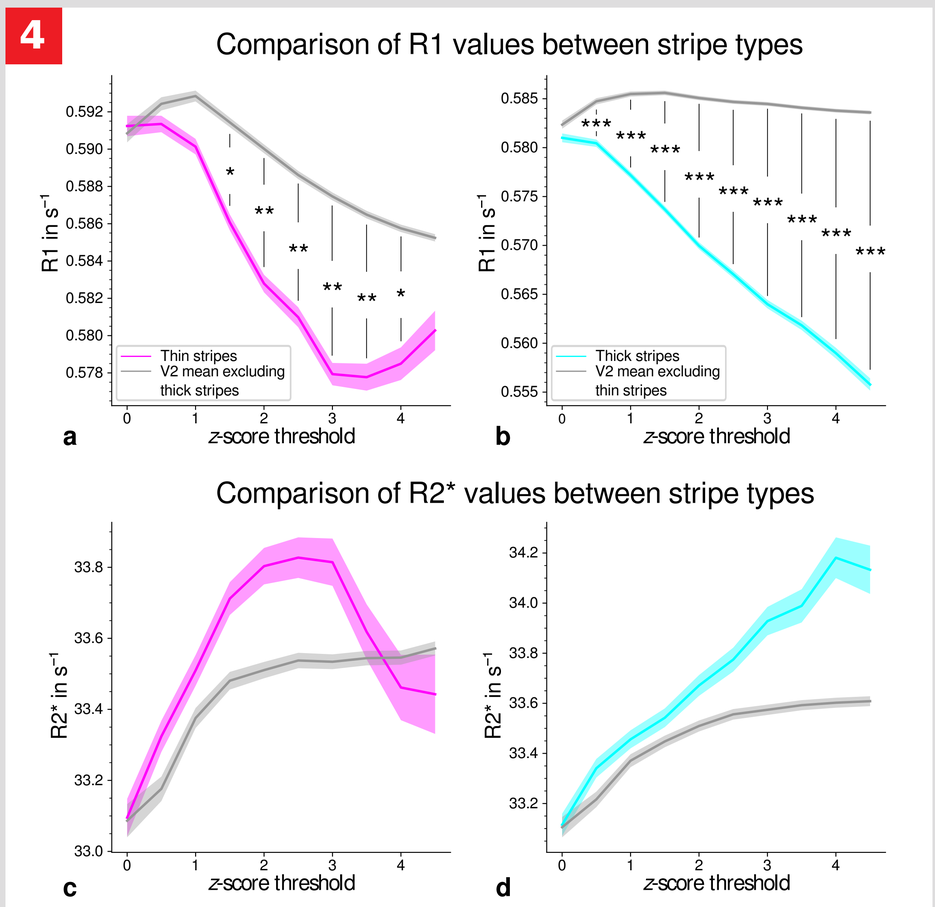
Robust mapping of thin and thick stripes in V2 — Activation maps of color-selective thin (a) and disparity-selective thick (b) stripes are shown for one representative participant. Maps are averaged across two sessions and sampled at mid-cortical depth using the equi-volume model [8]. Stripes running perpendicular to the V1/V2 border can be identified. Cyan dots are shown to illustrate the alternating stripe pattern in (a) vs. (b). Borders were manually defined based on separate retinotopy measurements. Black asterisks indicate the foveal region. RH: right hemisphere.

3



Cortical R1 sampled at mid-cortex — Data from one participant is shown in lateral (a) and posterior (b) view. Higher R1 values can be identified in primary motor and sensory areas as expected from the known heavier myelination of these areas. (c) Differences of mean R1 values between different cortical regions (angular gyrus, MT, V2, V1) defined by corresponding FreeSurfer labels for each participant also demonstrate the heavier myelination of V1 for all participants. Gray line: Mean across participants. Shaded area: 1 SD across participants.

4



Heavier myelination in pale stripes — Mean R1 (a)-(b) and R2* (c)-(d) values in thin (magenta) stripes, thick (cyan) stripes and whole V2 (gray) for several z-score threshold levels. The mean was computed across participants and hemispheres. Thin and thick stripe labels were defined by thresholding activation maps (see Fig. 2) at a specific z-score level. One stripe type was excluded in the definition for whole V2. Assuming a tripartite stripe division in V2, this allowed an indirect assessment of pale stripe contributions by comparing one stripe type to whole V2 excluding the other stripe type. [9] For each z = 0.0, 0.5, ..., 4.5, the difference between thin/thick stripes and whole V2 was tested for statistical significance using permutation testing. [10] We find lower R1 (but not R2*) values in thin and thick stripes which point to heavier myelination in pale stripes. Statistically significant differences are marked by asterisks, *: p<0.05, **: p<0.01, ***: p<0.001. Shaded area: 1 SEM.

Discussion

- Our results show that pale stripes in human V2 are heavier myelinated than surrounding gray matter which is in line with a recent MRI study in macaques. [9]
- Furthermore, we used qMRI parameter maps (R1, R2*) which are less biased by instrumental artefacts and better comparable across time, subjects and scanner sites than weighted images.
- This might be crucial to reliably measure small signal differences over larger cortical areas.
- To the best of our knowledge, this is the first study which demonstrates the feasibility to infer myelination variations within a cortical area at the spatial scale of cortical columns in living humans using qMRI.

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